

First molecular detection and phylogenetic analyses of *Neospora caninum* from naturally infected sheep in North Africa

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Abstract

Neospora caninum is a protozoan parasite from the phylum Apicomplexa. This parasite is as one of the major causative abortive agents in the dairy cattle industry. Moreover, abortions in sheep due to *N. caninum* have been reported by several studies (Moreno et al, 2012). The objective of this study was to estimate the molecular prevalence and phylogenetic analyses of *N. caninum* in Tunisian sheep.

A total number of 198 meat samples were collected from slaughtered ewes and tested for the presence of *N. caninum* ITS1 gene using PCR followed by sequencing of some PCR products. A phylogenetic tree was then constructed to compare the partial sequences of the ITS1 gene with GenBank sequences. The overall *N. caninum* infection prevalence rate in sheep was 10.6±4.3% (21/198). The infection rate was significantly higher for animals aged over one year (19.4±9.1%) when compared to those under one year of age (5.6±4) (p<0.001). The highest prevalence was observed in North Béja locality (31.2±16.1) (p<0.001). Compared to Barbarine (6.8±4.5%) and Cross-bred animals (0%), Noire de Thibar was the most infected

sheep breed ($31.7\pm 14.2\%$) ($p < 0.001$). Comparison of the partial sequences of the ITS1 gene revealed 96-98% similarity among our *N. caninum* amplicon and these deposited in GenBank.

To our knowledge this is the first molecular study and phylogenetic analysis of *N. caninum* in sheep in North Africa. Our results indicate the meat harbour *N. caninum* cysts and can contribute to a better evaluation of *N. caninum* infection and the associated abortions in sheep.